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DT   24-JUL-2002 (Rel. 72, Last updated, Version 2)
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RA   Ala'Aldeen D.A.;
RT   ;
RL   Submitted (13-MAR-2001) to the EMBL/GenBank/DDBJ databases.
RL   Ala'Aldeen D.A., Microbiology, University of Nottingham, University
RL   Hospital, Nottingham, NG7 2UH, UNITED KINGDOM.
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RX   MEDLINE; 22112893.
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RA   Turner D., Wooldridge K.G., Ala'Aldeen D.A.A.;
RT   "Autotransported serine protease A of Neisseria meningitidis: an
RT   immunogenic, surface-exposed outer membrane, and secreted protein.";
RL   Infect. Immun. 70(8):4447-4461(2002).
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RX   PUBMED; 8254661.
RA   Klauser T., Kraemer J., Otzelberger K., Pohlner J., Meyer T.F.;
RT   "Characterization of the Neisseria Iga beta-core. The essential unit for
RT   outer membrane targeting and extra";
RL   J. Mol. Biol. 234(3):579-593(1993).
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RA   Klauser T.;
RT   ;
RL   Submitted (02-FEB-1993) to the EMBL/GenBank/DDBJ databases.
RL   Thomas Klauser Dr., Infektionsbiologie, Max-Planck-Institut fuer, Biologie,
RL   Spemannstr. 34, Tuebingen, BW, W-7400, Germany
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1: X04835. Neisseria gonorrh...[gi:44868]

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VERSION     X04835.1  GI:44868
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  TITLE     Gene structure and extracellular secretion of Neisseria gonorrhoeae
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NiceProt View of TrEMBL: Q06467

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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**Q06467**
Primary accession number	**Q06467**
Secondary accession numbers	None
Entered in TrEMBL in	Release 01, November 1996
Sequence was last modified in	Release 01, November 1996
Annotations were last modified in	Release 24, June 2003

Name and origin of the protein

Protein name	**IgA-specific serine endopeptidase [Fragment]**
Synonyms	**EC 3.4.21.72** **IgA protease**
Gene name	None
From	Neisseria gonorrhoeae [TaxID: 485]
Taxonomy	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=R16;
MEDLINE=94076337; PubMed=8254661; [NCBI, ExPASy, EBI, Israel, Japan]
Klauser T., Kraemer J., Otzelberger K., Pohlner J., Meyer T.F.;
"Characterization of the Neisseria Iga beta-core. The essential unit for outer membrane targeting and extracellular protein secretion.";
J. Mol. Biol. 234:579-593(1993).

Comments

FUNCTION: THIS PROTEASE IS SPECIFIC FOR IMMUNOGLOBULIN A.
CATALYTIC ACTIVITY: CLEAVAGE OF IMMUNOGLOBULIN A MOLECULES AT CERTAIN PRO-|-XAA BONDS IN THE HINGE REGION. NO SMALL MOLECULE SUBSTRATES ARE KNOWN.
MISCELLANEOUS: IGA PROTEASE IS EXCRETED, THE SIGNAL PEPTIDE GUIDE THE IGA PRECURSOR TO THE PERIPLASMIC SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH

THE OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS.

Cross-references	
EMBL	Z21615; CAA79739.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence] Z21616; CAA79740.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence]
PIR	S31831; S31831.
GO	GO:0016021; Cellular component: integral to membrane *(inferred from electronic annotation).* GO:0016787; Molecular function: hydrolase activity *(inferred from electronic annotation).* GO:0004252; Molecular function: serine-type endopeptidase activity *(inferred from electronic annotation).*
InterPro	IPR006315; Autotransport. IPR005546; Autotransporter. Graphical view of domain structure.
Pfam	PF03797; Autotransporter; 1.
TIGRFAMs	TIGR01414; autotrans_barl; 1.
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	Q06467.
PRESAGE	Q06467.
ModBase	Q06467.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords
Hydrolase; **Serine protease**; **Zymogen**; **Transmembrane**.

Features

Feature table viewer

Key	From	To	Length	Description
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NON_TER	370	370		

Sequence information

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Q06467 in FASTA format

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BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Pr t

Hosted by NCSC US	Mirror sites:	Bolivia	Canada	China	Korea	Switzerland	Taiwan

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SV   Z21615.1
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DT   11-AUG-1995 (Rel. 44, Last updated, Version 6)
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KW   Igab-domain of IgA protease precursor.
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OC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae;
OC   Neisseria.
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RA   Klauser T., Kraemer J., Otzelberger K., Pohlner J., Meyer T.F.;
RT   "Characterization of the Neisseria Igab-core, the essential unit for outer
RT   membrane targeting and extracellular protein secretion.";
RL   J. Mol. Biol. 0:0-0(1993).
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RA   Klauser T.;
RT   ;
RL   Submitted (02-FEB-1993) to the EMBL/GenBank/DDBJ databases.
RL   Thomas Klauser Dr., Infektionsbiologie, Max-Planck-Institut fuer, Biologie,
RL   Spemannstr. 34, Tuebingen, BW, W-7400, Germany
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RN   [3]
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RX   PUBMED; 8254661.
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RT   "Characterization of the Neisseria Iga beta-core. The essential unit for
RT   outer membrane targeting and extra";
RL   J. Mol. Biol. 234(3):579-593(1993).
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INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 96/01130

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	VACCINE, vol. 12, no. 6, May 1994, pages 492-498, XP000651455 RUPPERT, A. ET AL.: "OmpA-FMDV VP1 fusion proteins: production, cell surface exposure and immune responses to the major antigenic domain of foot-and-mouth disease virus"	21,36,37
Y	see the whole document	1,2,9, 10,15, 16,38

X	EMBO J., vol. 11, no. 6, 1992, pages 2327-2335, XP002028468 KLAUSER, T. ET AL.: "Selective extracellular release of cholera toxin B subunit by Escherichia coli: dissection of Neisseria IgaA-mediated outer membrane transport" see the whole document	21,36,37

Y	MOLECULAR MICROBIOLOGY, vol. 18, no. 2, 1995, pages 377-382, XP000651438 JOSE, J. ET AL.: "MicroCorrespondence: Common structural featues of IgA1 protease-like outer membrane protein autotransporters" see page 378 - page 380	1-3, 5-10, 20-23, 38-40

Y	WO 93 10214 A (GEORGIOU, G.) 27 May 1993 see page 6, line 6 - page 10, line 28 see page 12, line 4 - page 13, line 29	1-25

Y	BIO-TECHNOLOGY, vol. 14, no. 2, February 1996, pages 203-208, XP002028469 CORNELIS, P. ET AL.: "Development of new cloning vectors for the production of immunogenic outer membrane fusion proteins in Escherichia coli" see the whole document	1,2,9-11

Y	MOLECULAR MICROBIOLOGY, vol. 17, no. 1, 1995, pages 123-135, XP000651454 BENJELLOUN-TOUIMI, Z. ET AL.: "SepA, the major extracellular protein of Shigella flexneri: autonomous secretion and involvement in tissue invasion" see the whole document	2,4

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Form PCT ISA 210 (continuation of second sheet) (July 1992)

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L2	(autotransporter$ or auto-transporter$) near25 neisser$	1	L2

END OF SEARCH HISTORY

1: Nature. 1987 Jan 29-Feb 4;325(6103):458-62.

nature

Gene structure and extracellular secretion of N gonorrhoeae IgA protease.

Pohlner J, Halter R, Beyreuther K, Meyer TF.

Several human bacterial pathogens, including the Gram-n diplococcus Neisseria gonorrhoeae, produce extracellular that are specific for human immunoglobulin IgA1. Immun (IgA) proteases have been studied extensively and the g some species cloned in Escherichia coli, but their role in pathogenesis remains unclear. Recently we derived a DN of 5 kilobases (kb) from N. gonorrhoeae MS11 directing extracellular active enzyme in E. coli. Although the matur of strain MS11 was shown to have a relative molecular mo 106,000 (Mr 106K) in gels, the DNA sequence of this clo fragment reveals a single gene coding for a 169K precurs protease. The precursor contains three functional domai amino-terminal leader which is assumed to initiate the in membrane transport of the precursor, the protease, and carboxyl-terminal 'helper' domain apparently required fo extracellular secretion (excretion). Based on the structu features of the precursor, we propose a model in which t serves as a pore for excretion of the protease domain th outer membrane. IgA protease acquires an active confor

outer membrane. IgA protease acquires an active conformation its extracellular transport proceeds and is released as a from the membrane-bound helper by autoproteolysis. The proform further matures into the 106 K IgA protease and stable alpha-protein.

PMID: 3027577 [PubMed - indexed for MEDLINE]

1: Trends Microbiol. 1998 Sep;6(9):370-8. Related Art

Full Text on BioMedNet GO

Entrez PubMed

The great escape: structure and function of th autotransporter proteins.

Henderson IR, Navarro-Garcia F, Nataro JP.

Dept of Medicine, University of Maryland School of Med Baltimore 21201, USA.

PubMed Services

The autotransporters, a family of secreted proteins fror Gram-negative bacteria, possess an overall unifying struc comprising three functional domains: the amino-terminal sequence, the secreted mature protein (passenger domai carboxy-terminal (beta-) domain that forms a beta-barre allow secretion of the passenger protein. Members of thi have been implicated as important or putative virulence f many Gram-negative pathogens.

Publication Types:

- Review
- Review, Tutorial

PMID: 9778731 [PubMed - indexed for MEDLINE]

Related Resources

Journal of Molecular Biology
Volume 234, Issue 3 , 5 December 1993, Pages 579-593

doi:10.1006/jmbi.1993.1613 Cite or link using doi

Regular Article

Characterization of the *Neisseria* Iga_{β}-core

The Essential Unit for Outer Membrane Targeting and Extracellular Protein Secretion

Thomas Klauser, Joachim Krämer, Karin Otzelberger, Johannes Pohlner and Thomas F. Meyer

Max-Planck-Institut für Biologie Abteilung Infektionsbiologie, Spemannstrasse 34 D-72076 Tübingen, Germany

Available online 29 April 2002.

Abstract

Extracellular transport of *Neisseria* IgA proteases across the bacterial outer membrane is accomplished by the translocation function contained within the

C-terminal Iga_β domain of IgA protease precursor proteins. Recently, we reported that Iga_β from *N. gonorrhoeae* MS11 (Val1097 to Phe1505), fused, to a periplasmic passenger protein, facilitated its transport across the outer membrane, leading to surface exposure of the passenger. In the present work we show, by systematic N-terminal truncation of Iga_β, that the functional and structural unit, termed Iga_β-core, corresponds to the C-terminal approximately 274 amino acid residues (Ser1231 to Phe1505). This minimal region retains all the essential features necessary for the translocation of an N-terminally attached passenger across the outer membrane of *Escherichia coli*, and for its own correct integration into the outer membrane, even in the absence of a passenger protein. The membrane-integrated Iga_β-core constitutes a conserved entity found in the C-terminal regions of Iga_β domains of different *N. gonorrhoeae, N. meningitidis* and *Haemophilus influenzae* strains. In contrast, the surface-exposed N termini of the Iga_β domains vary in size and sequence. Based on secondary structure predictions, the key structural feature of the core is a β-barrel (amphipathic, antiparallel transmembrane β-strands, interspersed by hairpin turns and loops) which is common to many integral outer membrane proteins of Gram-negative bacteria. We propose that the core has been conserved in evolution, to provide a selective outer membrane export channel for covalently attached polypeptides.

Author Keywords: IgA protease; protein secretion; Gram-negative; outer membrane protein; β-barrel

Journal of M lecular Biology
Volume 234, Issue 3 , 5 December 1993 , Pages 579-593

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